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(21) International Application Number: PCT/EP00/02053 (22) International Filing Date: 9 March 2000 (09.03.00) (30) Priority Data: 199 11 130.8 11 March 1999 (11.03.99) DE (71)(72) Applicant and Inventor: HAGER, Jörg [DE/FR]; 27, rue de Gien, F-91540 Mennecy (FR). (74) Agent: CABINET BECKER ET ASSOCIES; 10, rue de Milan, F-75009 Paris (FR).		(81) Designated States: CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS (57) Abstract The present invention relates to genetic mapping of complex quantitative and qualitative traits. This invention more particularly relates to compositions and methods to identify identical DNA fragments from two different DNA sources. The method allows the amplification of the DNA's, their labelling, and the separation of perfectly matched DNA's from imperfectly matched DNA's or from DNA's formed through hybridisation from the same source (e.g., homohybrids). The invention can be used to identify genes or gene mutations, which are relevant to pathological conditions or particular traits.		

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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, MEDLINE, CHEM ABS Data, BIOSIS, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 93 22457 A (MASSACHUSETTS INST TECHNOLOGY) 11 November 1993 (1993-11-11) the whole document	1-22
Y	US 5 750 335 A (GIFFORD DAVID K) 12 May 1998 (1998-05-12) the whole document	1-22
Y	WO 93 22462 A (UNIV LELAND STANFORD JUNIOR) 11 November 1993 (1993-11-11) See pages 15-16 the whole document	1-22
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Y	WO 89 12695 A (GENELABS INC) 28 December 1989 (1989-12-28) See page 12- page 16, fig.1 and fig.3 the whole document ---	1-22
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Claims

1. A method for the identification (or isolation or separation) of identical nucleic acid fragments from a mixture of at least two nucleic acid populations, comprising: a) separate digestion of the nucleic acids of
5 said at least two populations with at least one restriction enzyme; b) ligation of an adaptor sequence to the restriction fragments; c) amplification of the adaptor-ligated restriction fragments generated in a) and b) using an adaptor-specific primer; d) hybridisation of the
10 amplification products from the different nucleic acid populations with each other ; e) identification (or isolation or separation) of the identical, fully matched, heterohybrid fragments.
2. A method of claim 1, wherein the nucleic acid populations are
15 genomic DNA populations, preferably human genomic DNA populations, more preferably from different subjects having a common trait of interest.
3. Method of claim 1 or 2, wherein the nucleic acid populations
20 comprise selected chromosome(s).
4. Method of any one of claims 1 to 3, wherein two or more nucleic acid populations from different sources are used.
- 25 5. Method according to any one of the preceding claims, wherein the restriction fragments are size selected prior to the amplification reaction.
- 30 6. Method according to any one of the preceding claims, wherein part or all of the restriction fragments are cloned into a vector, in a chromosome- and sequence-specific fashion.

7. Method according to any one of claims 1 to 6, wherein the adaptor sequence comprises a recognition site for *mut* HL.
8. Method of claim 7, wherein the adaptor molecule is a 5-100 base long
5 double-stranded DNA fragment comprising at least one GATC motif.
9. Method according to any one of claims 1 to 8, wherein the amplification is a by polymerase chain reaction (PCR).
10. Method according to any one of claims 1 to 9, wherein the primer is
10 complementary to at least a part of the adaptor molecule sequence.
11. Method of claim 9, wherein the primer is labelled, preferably by (i) adding a unique 5'-sequence to each primer, (ii) adding a chemical
15 activity to the primer which provides a means to distinguish between the amplification products from different nucleic acid populations or (iii) adding modified nucleotides into the primer allowing to distinguish between the amplification products from different nucleic acid populations.
- 20 12. Method according to any one of the preceding claims, wherein the identification of matched heterohybrids comprises a (i) separation of homoduplexes from heteroduplexes; (ii) (identification and) elimination of mismatched heterohybrids, and (iii) identification (or isolation or
25 separation) of the identical heterohybrid fragments.
13. Method of claim 12., wherein the heterohybrids are separated from the homohybrids based on labelling of primers.
- 30 14. Method of claim 13, comprising a) separate amplification of the restriction fragments using a primer with a unique 5' sequence for each nucleic acid population; b) mixing the amplification products from said

different nucleic acid populations carrying unique 5' ends; c) denaturation and rehybridizing said nucleic acids; d) digesting perfectly matched (blunt ended) DNA's (homoduplexes) by *Exo III* and e) elimination of the *Exo III* created single strands, preferably through
5 binding to a single strand specific matrix.

15. Method of claim 12, wherein the heterohybrids are separated from the homohybrids based on the methylation of one of the two nucleic acid preparations (or restriction fragments).

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16. Method of claim 12, wherein mismatched heterohybrids are eliminated with mismatch repair enzymes.

17. Method of claim 16, wherein mismatched nucleic acid fragments are
15 eliminated by (i) incubating the hybridisation mixture with *MutS* and (ii) contacting the resulting product with a *MutS*-binding material.

18. Method of claim 16, wherein mismatched nucleic acid fragments are eliminated by incubating the hybridisation mixture with *MutS*, *MutL*
20 and *MutH*, resulting in a specific cleavage of mismatched hybrids.

19. A kit suitable for genetic analysis in accordance with claim 1, comprising a double stranded adaptor molecule, a specific labelled primer and, optionally, control DNA's and enzymes.

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20. Kit of claim 19, further comprising a means for the detection of the selected DNA fragments, preferably an ordered DNA array or coded beads carrying specific DNA sequences.

30 21. A method of separating identical DNA fragments from complex mixtures of at least two nucleic acid populations, comprising hybridizing the at least two populations and separating the identical

heterohybrids formed, wherein the nucleic acid populations comprise amplified nucleic acids.

22. A method to identify DNA regions that are relevant to a pathological
5 condition or a particular trait, comprising hybridizing at least two
nucleic acid populations from different sources having the particular
trait or pathology, and separating the identical heterohybrids formed
which contain DNA regions that are relevant to said pathological
condition or particular trait, wherein the nucleic acid populations
10 comprise amplified and/or pre-selected nucleic acids.